IN THE SPECIFICATION:

Please amend the specification as shown:

Please delete Table 2 and replace it with the following Table:

Table 2

Tm	length	name	probe sequence 5'-3'	SEQ ID NO:
52.7	18	process control	AGAAACGCTGGTGAAAGT	1
45.6	18	neg. hybridization	TCTAGACAGCCACTCATA	2
58.0	18	pos. hybridization	GATTGGACGAGTCAGGAGC	3
45.6	18	spot control	Cy5-TCTAGACAGCCACTCATA	4
56.4	22	S04	ATGAGTATTNAACATTTCCGTG	5
59.9	20	S19	GCATTTTGCNTTCCTGTTTT	6
56.3	19	S37	CTGAAGATNAGTTGGGTGC	7
66.8	21	S40	CAGTTGGGTGNACGAGTGGGT	8
72.4	27	S49	ATCGAACTGGATCNCAACAGCGGTAAG	9
66.1	26	S67	CGTTTTCCAATGNTGAGCACTTTTAA	10
59.9	24	S67.2	TTTTCCAATGATNAGCACTTTTAA	11
64.0	20	S78*	ATGTGGTGCGGNATTATCCC	12
62.8	19	S82*	TTATCCCGTNTTGACGCCG	13
68.3	17	S90	GCAACTCGNTCGCCGCA	14
51.4	20	S102	GACTTGGTTNAGTACTCACC	15
58.1	19	S113	ATCTTACGGNTGGCATGAC	16
59.6	22	S122	AGAATTATGCANTGCTGCCATA	17
58.9	18	S125	GTGCTGCCNTAACCATGA	18
64.8	24	S127	TGCCATAACCATGNGTGATAACAC	19
62.1	17	S143*	CGGAGGANCGAAGGAGC	20
76.7	24	S151	CCGCTTTTTTGCNCAACATGGGGG	21
66.9	19	S161*	CTCGCCTTGNTCGTTGGGA	22
57.5	17	S162	GCCTTGATNGTTGGGAA	23
62.6	19	162.2	GCCTTGATCNTTGGGAACC	24
61.3	17	S163	TTGATCGTNGGGAACCG	25
64.3	19	S163.2	TGATCGTTGNGAACCGGAG	26
55.6	17	S180	CACCACGANGCCTGTAG	27
67.4	19	S182	CGATGCCTGNAGCAATGGC	28
53.3	23	194.2	AACTATTAACTNGCGAACTACTT	29
51.7	22	194	ACTATTAACTGNCGAACTACTT	30
62.4	22	S202	CTAGCTTCCCNGCAACAATTAA	31
52.4	18	S216	AGTTGCAGNACCACTTCT	32
62.5	19	235.2	AAATCTGGANCCGGTGAGC	33
59.6	17	235	ATCTGGAGNCGGTGAGC	34
63.6	17	236	CTGGAGCCNGTGAGCGT	35
66.6	18	236.2	CTGGAGCCGNTGAGCGTG	36
67.2	18	S237	GAGCCGGTNAGCGTGGGT	37
56.9	17	241	GTGGGTCTNGCGGTATC	38
60.7	19	241.2	GTGGGTCTCNCGGTATCAT	39
54.0	22	S258	CCGTATCGTANTTATCTACACG	40
53.4	18	S261	TTATCTACANGACGGGGA	41
69.3	17	S264	CGACGGGGNGTCAGGCA	42
53.9	21	S271	ATGGATGAACNAAATAGACAG	43
52.9	21	S272	GGATGAACGANATAGACAGAT	44
58.1	23	S276	TAGACAGATCGNTGAGATAGGTG	45

Probe sequence table for the TEM array. The probe sequence is given from 5' to 3'.
The triplet with the amino acid substitution is underlined.
For each SNP position (named after the position in the amino acid sequence of *blaTEM)* 4 probes exist with either A, G, C or T at the central base position, marked as N in the probe sequence.
Also indicated for each probe is the probe length (between 17-27 bases) and the melting temperature (calculated for probes with central base = G; 50 nM DNA conc, 50 mM salt conc., as described by Breslauer et al., Proc. Nat. Acad. Sci. 83, 3746-50, 1986). (* probes = with 15 thymidin spacer)

Please delete paragraph [0072] and replace it with the following paragraph:

[0001]Target DNA was synthesized by PCR. The amplification primers for the blaTEM genes were temforw (5'-atgagtattcaacatttccg-3')**(SEQ ID NO: 46)** and temrev (5'-ttaatcagtgaggcacctat-3') **(SEQ ID NO: 47)**. For PCR amplification and labeling 1-75 ng of plasmid DNA was supplemented with 100 μl PCR-buffer (2.5 mM $Mg(OAc)_2$, 50 mM KCl, 10 mM Tris-HCl pH 8.3) containing 50 μM dATP, dGTP, dTTP, 30 μM dCTP, 20 μM Cy5-dCTP; Amersham Biosciences, Little Chalfont, UK) and 10 U Taq DNA Polymerase (Eppendorf AG, Hamburg, Germany). Amplification was performed in a Mastercycler Gradient (Eppendorf AG, Hamburg, Germany). An initial denaturation step (94°C for 1 min) was followed by 30 cycles (94°C for 30 s, 55°C for 30 s, 72°C for 1 min) and a final extension step at 72°C for 4 min.